



SEQUENCE LISTING

<110> DAI, KEN-SHW0
 <120> HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER
 <130> U014798-3
 <140> 10/653,681
 <141> 2003-09-02
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 <170> PatentIn version 3.2
 <210> 1
 <211> 1090
 <212> DNA
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

<220>
 <221> CDS
 <222> (70)..(333)

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 gcaccaacc atg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc 111
 Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
 1 5 10
 att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa 159
 Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
 15 20 25 30
 gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc 207
 Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
 35 40 45
 tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag 255
 Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
 50 55 60
 atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag 303
 Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
 65 70 75
 ttg tgg ccc act tcc aga tcg aga agc tct tgaacaaacc tggactgaaa 353
 Leu Trp Pro Thr Ser Arg Ser Arg Ser Ser
 80 85
 tataaaccag tgactaacca gggtgagtgt cacccatacc tcacgcagga gaaactgac 413
 cagtactgcc actccaaggg catcaccgtt acggcctaca gccccctggg ctctccggat 473
 agaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt 533

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gctgcaaagc acaaaaaaac cgcagcccag gttctgatcc gtttccatat ccagaggaat 593
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gactttaaat tgagtgatga ggagatggca accataactca gcttcaacag aaactggagg 713
gcctgtaacg tgttgcaatc ctctcatttg gaagactatc ctttcgatgc agaattattga 773
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aatatcacag aaaagcatgg cttgaataag gaaatgacaa ttttttccac ttatctgatc 1013
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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
          20          25          30

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Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
          35          40          45

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Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
          50          55          60

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Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
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Pro Thr Ser Arg Ser Arg Ser Ser
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<210> 3
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<222> (70)..(804)

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      Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
      1              5              10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa      159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15              20              25              30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc      207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
      35              40              45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag      255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
      50              55              60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag      303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
      65              70              75

ttg tgg ccc act ttc ttt gag aga ccc ctt gtg agg aaa gcc ttt gag      351
Leu Trp Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu
      80              85              90

aag acc ctc aag gac ctg aag ctg agc tat ctg gac gtc tat ctt att      399
Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile
      95              100              105              110

cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat      447
His Trp Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp
      115              120              125

gat aaa ggt aat gcc atc ggt gga aaa gca acg ttc ttg gat gcc tgg      495
Asp Lys Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp
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gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg      543
Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly
      145              150              155

gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct      591
Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro
      160              165              170

gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac      639
Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr
      175              180              185              190
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ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc 687
 Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr 205
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gtt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag 735
 Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys 220
 210

cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct 783
 Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala 235
 225

gca aag cac tcc cca agt ctg tgacaccagc acgcattggt gagaacattc 834
 Ala Lys His Ser Pro Ser Leu 245
 240

aggtctttga ctttaaattg agtgatgagg agatggcaac catactcagc ttcaacagaa 894
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<210> 4
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 <212> PRT
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<220>
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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val
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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
 20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
 50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp

65		70		75		80									
Pro	Thr	Phe	Phe	Glu 85	Arg	Pro	Leu	Val	Arg 90	Lys	Ala	Phe	Glu	Lys 95	Thr
Leu	Lys	Asp	Leu 100	Lys	Leu	Ser	Tyr	Leu 105	Asp	Val	Tyr	Leu	Ile 110	His	Trp
Pro	Gln	Gly 115	Phe	Lys	Ser	Gly	Asp 120	Asp	Leu	Phe	Pro	Lys 125	Asp	Asp	Lys
Gly	Asn 130	Ala	Ile	Gly	Gly	Lys 135	Ala	Thr	Phe	Leu	Asp 140	Ala	Trp	Glu	Ala
Met 145	Glu	Glu	Leu	Val	Asp 150	Glu	Gly	Leu	Val	Lys 155	Ala	Leu	Gly	Val	Ser 160
Asn	Phe	Ser	His	Phe 165	Gln	Ile	Glu	Lys	Leu 170	Leu	Asn	Lys	Pro	Gly 175	Leu
Lys	Tyr	Lys	Pro 180	Val	Thr	Asn	Gln	Val 185	Glu	Cys	His	Pro	Tyr 190	Leu	Thr
Gln	Glu	Lys 195	Leu	Ile	Gln	Tyr	Cys 200	His	Ser	Lys	Gly	Ile 205	Thr	Val	Thr
Ala	Tyr 210	Ser	Pro	Leu	Gly	Ser 215	Pro	Asp	Arg	Pro	Trp 220	Ala	Lys	Pro	Glu
Asp 225	Pro	Ser	Leu	Leu	Glu 230	Asp	Pro	Lys	Ile	Lys 235	Glu	Ile	Ala	Ala	Lys 240
His	Ser	Pro	Ser	Leu 245											